

#3



1/24

## SEQUENCE LISTING

*Jub  
PO*

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Huang, Yung-Sheng  
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Thurmond, Jennifer M.  
Pereira, Suzette L.  
Leonard, Amanda E.

<120> DESATURASE GENES AND USES THEREOF

<130> 6763.US.P1

<140> 10/054,534  
<141> 2002-01-22

<150> US 09/769,863  
<151> 2001-01-25

<160> 55

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<223> y = t/u or c at position 6

<221> misc\_feature  
<222> (9)...(9)  
<223> y = t/u or c at position 9

<221> misc\_feature  
<222> (12)...(12)  
<223> b = g or c or t/u at position 12

<221> misc\_difference  
<222> (18)...(18)  
<223> r = g or a at position 18

<221> misc\_feature  
<222> (24)...(24)  
<223> b = g or c or t/u at position 24

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<221> misc_feature
<222> (30)...(30)
<223> y = t/u or c at position 30

<221> misc_feature
<222> (33)...(33)
<223> y = t/u or c at position 33

<221> misc_feature
<222> (36)...(36)
<223> b = g or c or t/u at position 36

<221> misc_feature
<222> (39)...(39)
<223> h = a or c or t/u at position 39

<221> misc_feature
<222> (42)...(42)
<223> h = a or c or t/u at position 42

<400> 1
gtbtaygayg tbaccgartyg ggtbaagcgy cayccbgghg gh
<210> 2
<211> 45
<212> DNA
<213> Artificial Sequence

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<223> Forward Primer R0835

<221> misc_feature
<222> (3)...(3)
<223> h = a or c or t/u at position 3

<221> misc_feature
<222> (6)...(6)
<223> y = t/u or c at position 6

<221> misc_feature
<222> (12)...(12)
<223> y = t/u or c at position 12

<221> misc_feature
<222> (27)...(27)
<223> y = t/u or c at position 27

<221> misc_feature
<222> (33)...(33)
<223> y = tu or c at position 33

<221> misc_feature
<222> (39)...(39)
<223> b = g or c or t/u at position 39

<221> misc_feature
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<222> (41)...(41)
<223> y = t/u or c at position 41

<221> misc_feature
<222> (45)...(45)
<223> y = t/u or c at position 45

<400> 2
gg hgc ytccg cyaactggtg gaagcaycag cayaacgtbc aycay 45
<210> 3
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer R0836

<221> misc_feature
<222> (1)...(1)
<223> r = g or a at position 1

<221> misc_feature
<222> (4)...(4)
<223> r = g or a at position 4

<221> misc_feature
<222> (7)...(7)
<223> v = a or g or c at position 7

<221> misc_feature
<222> (13)...(13)
<223> r = g or a at position 13

<221> misc_feature
<222> (19)...(19)
<223> r = g or a at position 19

<221> misc_feature
<222> (34)...(34)
<223> r = g or a at position 34

<221> misc_feature
<222> (40)...(40)
<223> r = g or a at position 40

<221> misc_feature
<222> (43)...(43)
<223> d = a or g or t/u at position 43

<400> 3
rtgrtgvacg ttrtgctgrt gcttccacca gttrgcggar gcdcc 45
<210> 4
<211> 36
<212> DNA
<213> Artificial Sequence

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<220>
<223> Reverse Primer R0838

<221> misc_feature
<222> (6)...(6)
<223> r = g or a at position 6

<221> misc_feature
<222> (12)...(12)
<223> r = g or a at position 12

<221> misc_feature
<222> (15)...(15)
<223> y = t/u or c at position 15

<221> misc_feature
<222> (18)...(18)
<223> r = g or a at position 18

<221> misc_feature
<222> (21)...(21)
<223> r = g or a at position 21

<221> misc_feature
<222> (24)...(24)
<223> s = g or c at position 24

<221> misc_feature
<222> (27)...(27)
<223> r = g or a at position 27

<221> misc_feature
<222> (30)...(30)
<223> v = a or g or c at position 30

<400> 4
ttgatrgtct arctygtrgt rgasaarggv tggtac
<210> 5
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer R0753

<221> misc_feature
<222> (10)...(10)
<223> n = a or g or c or t/u, unknown, or other at
      position 10

<221> misc_feature
<222> (13)...(13)
<223> r = g or a at position 13

<221> misc_feature

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<222> (16)...(16)
<223> n = a or g or c or t/u, unknown, or other at
      position 16

<221> misc_feature
<222> (18)...(19)
<223> r = g or a at positions 18-19

<221> misc_feature
<222> (22)...(22)
<223> r = g or a at position 22

<400> 5
catcatcatn ggraanarrt grtg

<210> 6
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO754

<221> misc_feature
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<223> y = t/u or c at position 15

<221> misc_feature
<222> (18)...(18)
<223> y = t/u or c at position 18

<221> misc_feature
<222> (21)...(21)
<223> n = a or g or c or t/u, unknown, or other at
      position 21

<221> misc_feature
<222> (24)...(24)
<223> y = t/u or c at position 24

<221> misc_feature
<222> (27)...(27)
<223> n = a or g or c or t/u, unknown, or other at
      position 27

<221> misc_feature
<222> (30)...(30)
<223> y = t/u or c at position 30

<400> 6
ctactactac tacaycayac ntayacnaay

<210> 7
<211> 29
<212> DNA
<213> Artificial Sequence

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24

30

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<223> Primer RO923		
<400> 7		
cggtgcagtg gtgaaagaac aagcacaac	29	
<210> 8		
<211> 30		
<212> DNA		
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<220>		
<223> Primer RO899		
<400> 8		
agcggataac aatttcacac aggaaacagc	30	
<210> 9		
<211> 30		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Primer RO939		
<400> 9		
cgtatctactg ctcgaggagc ttgagcgccg	30	
<210> 10		
<211> 31		
<212> DNA		
<213> Artificial Sequence		
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<223> Primer RO898		
<400> 10		
cccagtcacg acgttgtaaa acgacggcca g	31	
<210> 11		
<211> 45		
<212> DNA		
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<223> Primer RO951		
<400> 11		
tcaacagaat tcatggtcca ggggcaaaag gccgagaaga tctcg	45	
<210> 12		
<211> 47		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Primer RO960		

<400> 12  
 atacgtaaacg ttttacatgg cggaaaactc cttgaagaac tcgatcg 47

<210> 13  
 <211> 1362  
 <212> DNA  
 <213> Saprolegnia diclina

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 caagacaacg cgtggatcgat gatcaccac aagggtgtacg acatctcgcc ctttggggac 120  
 caccggggcg gctgcgtcat gttcacgcag gccggcgaag acgcgaccga tgcgttcgct 180  
 gtcttccacc cgagctcgcc gctcaagctc ctcgagcaat actacgtcgcc cgacgtcgac 240  
 cagtcgacgg cggccgtcga cacgtcgatc tcggacgagg tcaagaagag ccagtccggac 300  
 ttccattgcgt cgtaccgcaa gctgcgcctt gaagtcaagc gcctcggctt gtacgactcg 360  
 agcaagctc actaccctca caagtgcgc tcgacgtcgatc gcatcgctt tgggtcgcc 420  
 gcccatttgc tccactttga ctcgacggcc atgtacatgg tcgcccgtt catccttgc 480  
 ctcttttacc agcagtgcgg ctggctcgcc catgacttc tgaccacca agtgttttag 540  
 aaccacttgtt ttggcgaccc cgtccggcgtc atgggtcgcc acctctggca gggcttctcg 600  
 gtgcagtgtt ggaagaacaa gcacaacacg caccatgcga tcccccaacctt ccacgcgacg 660  
 cccgagatcg ccttccacgg cgaccggac attgacacga tgccgattct cgctgggtcg 720  
 ctcaagatgg cgccggcgtc ggtcgactcg cccgtcgcc tcttcttcat gctgttccaa 780  
 gctgtacctgt actttcccat tttgtctttt ggcgttatct cgtgggtgat ccagtcggcc 840  
 atgtacgcct tctacaacgt tggggccggc ggcaccttg acaaggtcca gtacccgctg 900  
 ctcgagcgcc cccgcctctt cctctactac ggctggaaacc tcggccttgcgt gtacgcagcc 960  
 aacatgtcgc tgctccaacgc ggctcggttc ctcttgcga qccaggcgcc gtgcggccctc 1020  
 ttcctcgcga tggcttttag cgtccggccac aacggcatgg aggtcttga caaggacacg 1080  
 aagcccgatt tttggaaagct gcaagtgcgc tcgacgcgc acgtgacgtc gtcgtctgg 1140  
 atcgactgtt tcatgggggg cctcaactac cagatcgacc accactgtt cccgatgggt 1200  
 ccccccgcaca acctcccgcc gctcaacgtc ctcgtcaagt cgctctgcaaa gcagtagc 1260  
 atcccatacc acgagacggg cttcatcgcc ggcacccggc aggtcgtcgatc gacacccgag 1320  
 cgcacccatcgatc tgcgttccaa caaggagttt cccgcatgt aa 1362

<210> 14  
 <211> 453  
 <212> PRT  
 <213> Saprolegnia diclina

<400> 14  
 Met Val Gln Gly Gln Lys Ala Glu Lys Ile Ser Trp Ala Thr Ile Arg  
 1 5 10 15  
 Glu His Asn Arg Gln Asp Asn Ala Trp Ile Val Ile His His Lys Val  
 20 25 30  
 Tyr Asp Ile Ser Ala Phe Glu Asp His Pro Gly Gly Val Val Met Phe  
 35 40 45  
 Thr Gln Ala Gly Glu Asp Ala Thr Asp Ala Phe Ala Val Phe His Pro  
 50 55 60  
 Ser Ser Ala Leu Lys Leu Leu Glu Gln Tyr Tyr Val Gly Asp Val Asp  
 65 70 75 80  
 Gln Ser Thr Ala Ala Val Asp Thr Ser Ile Ser Asp Glu Val Lys Lys  
 85 90 95  
 Ser Gln Ser Asp Phe Ile Ala Ser Tyr Arg Lys Leu Arg Leu Glu Val  
 100 105 110  
 Lys Arg Leu Gly Leu Tyr Asp Ser Ser Lys Leu Tyr Tyr Leu Tyr Lys  
 115 120 125  
 Cys Ala Ser Thr Leu Ser Ile Ala Leu Val Ser Ala Ala Ile Cys Leu

130	135	140													
His	Phe	Asp	Ser	Thr	Ala	Met	Tyr	Met	Val	Ala	Ala	Val	Ile	Leu	Gly
145						150				155					160
Leu	Phe	Tyr	Gln	Gln	Cys	Gly	Trp	Leu	Ala	His	Asp	Phe	Leu	His	His
						165				170					175
Gln	Val	Phe	Glu	Asn	His	Leu	Phe	Gly	Asp	Leu	Val	Gly	Val	Met	Val
						180				185					190
Gly	Asn	Leu	Trp	Gln	Gly	Phe	Ser	Val	Gln	Trp	Trp	Lys	Asn	Lys	His
						195				200					205
Asn	Thr	His	His	Ala	Ile	Pro	Asn	Leu	His	Ala	Thr	Pro	Glu	Ile	Ala
						210				215					220
Phe	His	Gly	Asp	Pro	Asp	Ile	Asp	Thr	Met	Pro	Ile	Leu	Ala	Trp	Ser
						225				230					240
Leu	Lys	Met	Ala	Gln	His	Ala	Val	Asp	Ser	Pro	Val	Gly	Leu	Phe	Phe
						245				250					255
Met	Arg	Tyr	Gln	Ala	Tyr	Leu	Tyr	Phe	Pro	Ile	Leu	Leu	Phe	Ala	Arg
						260				265					270
Ile	Ser	Trp	Val	Ile	Gln	Ser	Ala	Met	Tyr	Ala	Phe	Tyr	Asn	Val	Gly
						275				280					285
Pro	Gly	Gly	Thr	Phe	Asp	Lys	Val	Gln	Tyr	Pro	Leu	Leu	Glu	Arg	Ala
						290				295					300
Gly	Leu	Leu	Leu	Tyr	Tyr	Gly	Trp	Asn	Leu	Gly	Leu	Val	Tyr	Ala	Ala
						305				310					320
Asn	Met	Ser	Leu	Leu	Gln	Ala	Ala	Ala	Phe	Leu	Phe	Val	Ser	Gln	Ala
						325				330					335
Ser	Cys	Gly	Leu	Phe	Leu	Ala	Met	Val	Phe	Ser	Val	Gly	His	Asn	Gly
						340				345					350
Met	Glu	Val	Phe	Asp	Lys	Asp	Ser	Lys	Pro	Asp	Phe	Trp	Lys	Leu	Gln
						355				360					365
Val	Leu	Ser	Thr	Arg	Asn	Val	Thr	Ser	Ser	Leu	Trp	Ile	Asp	Trp	Phe
						370				375					380
Met	Gly	Gly	Leu	Asn	Tyr	Gln	Ile	Asp	His	His	Leu	Phe	Pro	Met	Val
						385				390					400
Pro	Arg	His	Asn	Leu	Pro	Ala	Leu	Asn	Val	Leu	Val	Lys	Ser	Leu	Cys
						405				410					415
Lys	Gln	Tyr	Asp	Ile	Pro	Tyr	His	Glu	Thr	Gly	Phe	Ile	Ala	Gly	Met
						420				425					430
Ala	Glu	Val	Val	Val	His	Leu	Glu	Arg	Ile	Ser	Ile	Glu	Phe	Phe	Lys
						435				440					445
Glu	Phe	Pro	Ala	Met											
						450									

<210> 15  
<211> 23  
<212> DNA  
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<220>  
<223> Primer R0851

<400> 15  
ccatcaagac gtaccttgcg atc

<210> 16  
<211> 28  
<212> DNA

<213> Artificial Sequence

<220>

<223> Primer R0941

<400> 16

gctgaacggg tggtacgagt cgaacgtg

<210> 17

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer R0953

<400> 17

acgagagaat tcatggcccc gcagacggag ctccgccagc gc

28

<210> 18

<211> 46

<212> DNA

<213> Artificial Sequence

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<223> Primer R0956

<400> 18

aaaagactcg agttagccca tgtggatcgt ggcggcgatg ccctgc

42

<210> 19

<211> 1413

<212> DNA

<213> Saprolegnia diclina

<400> 19

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 ggcagaagg cctttacatg gcaggaggc gcgcgcaca acacggcggc ctccggcctgg 120  
 atcatttatcc gccgcaggct ctacgcgtg accgagtggg ccaacaagca ccccgccggc 180  
 cgcgagatgg tgctgctgca cgccggctgc gaggccaccc acacgttcga ctgttaccac 240  
 ccgttcagcg acaaggccga gtcgatcttg aacaagtatg agatggcac gttcacgggc 300  
 ccgtcccgat ttccgaccc caagccggac acgggcttct acaaggagtg cgcgaagcgc 360  
 gttggcgatg acttcaagaa gaacaacccatc catccgcagg acggcttccc gggctctgg 420  
 cgcatgtgg tcgtgtttgc ggtgcggc ctgcgcctgt acggcatgca ttttcgact 480  
 atctttgcgc tgcaagctcgc ggccgcggcg ctctttggcg tctgccaggc gctgccgtg 540  
 ctccacgtca tgcaacgtc gtcgcacgcg tcgtacacca acatccgtt cttccattac 600  
 gtcgtcgccgc gcttgcctat ggactggtt gccggcggtc cgatgggtgc atggctcaac 660  
 cagcacgtcg tgggccacca catctacacg aacgtcgccg gctccggaccc ggtatcttcg 720  
 gtcaacatgg acggcgacat ccgcgcgcgcgtc gtgaaccggc aggtgttcca gcccacgtac 780  
 gcattccagc acatctacat tccggcgctc tatggcggtc ttggcctcaa gttccgcac 840  
 caggacttca ccgcacacgtt cggctcgac acgaacggcc cgatccgcgt caacccgcac 900  
 ggcgcgcgcgtc cgtggatggc catgatcgc tccaagtctgt tctggccctt ctaccgcgtg 960  
 tacottccgc ttgcccgtgt ccagatgccc atcaagacgt accttgcgtat cttcttcctc 1020  
 gcccggatggtgcgtc gtacccgtcg tcaacttcc aagtaagcca tgcgtcgacc 1080  
 gagtgccggct acccatgcgg cgacgaggcc aagatggcgc tccaggacga gttggcgatc 1140  
 tcgcaggatca agacgtcggt cgactacgac catggctctgt ggtatgcac gttcccttgc 1200  
 ggcgcgcgtca actaccaggat cgtgcaccac ttgttccca gctgtcgca gtaccactac 1260

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ccggcgatcg cgcccatcat cgtcgacgac tgcaaggagt acaacatcaa gtacgccatc 1320  
 ttgccggact ttacggcggc gttcggtgcc cacttgaagc acctccgcaa catgggccag 1380  
 cagggcatcg cgcacatggc taa 1413

<210> 20  
 <211> 470  
 <212> PRT  
 <213> Saprolegnia diclina

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 1 5 10 15  
 Thr Pro Val Ala Gly Lys Ala Phe Thr Trp Gln Glu Val Ala Gln  
 20 25 30  
 His Asn Thr Ala Ala Ser Ala Trp Ile Ile Ile Arg Gly Lys Val Tyr  
 35 40 45  
 Asp Val Thr Glu Trp Ala Asn Lys His Pro Gly Gly Arg Glu Met Val  
 50 55 60  
 Leu Leu His Ala Gly Arg Glu Ala Thr Asp Thr Phe Asp Ser Tyr His  
 65 70 75 80  
 Pro Phe Ser Asp Lys Ala Glu Ser Ile Leu Asn Lys Tyr Glu Ile Gly  
 85 90 95  
 Thr Phe Thr Gly Pro Ser Glu Phe Pro Thr Phe Lys Pro Asp Thr Gly  
 100 105 110  
 Phe Tyr Lys Glu Cys Arg Lys Arg Val Gly Glu Tyr Phe Lys Lys Asn  
 115 120 125  
 Asn Leu His Pro Gln Asp Gly Phe Pro Gly Leu Trp Arg Met Met Val  
 130 135 140  
 Val Phe Ala Val Ala Gly Leu Ala Leu Tyr Gly Met His Phe Ser Thr  
 145 150 155 160  
 Ile Phe Ala Leu Gln Leu Ala Ala Ala Leu Phe Gly Val Cys Gln  
 165 170 175  
 Ala Leu Pro Leu Leu His Val Met His Asp Ser Ser His Ala Ser Tyr  
 180 185 190  
 Thr Asn Met Pro Phe Phe His Tyr Val Val Gly Arg Phe Ala Met Asp  
 195 200 205  
 Trp Phe Ala Gly Gly Ser Met Val Ser Trp Leu Asn Gln His Val Val  
 210 215 220  
 Gly His His Ile Tyr Thr Asn Val Ala Gly Ser Asp Pro Asp Leu Pro  
 225 230 235 240  
 Val Asn Met Asp Gly Asp Ile Arg Arg Ile Val Asn Arg Gln Val Phe  
 245 250 255  
 Gln Pro Met Tyr Ala Phe Gln His Ile Tyr Leu Pro Pro Leu Tyr Gly  
 260 265 270  
 Val Leu Gly Leu Lys Phe Arg Ile Gln Asp Phe Thr Asp Thr Phe Gly  
 275 280 285  
 Ser His Thr Asn Gly Pro Ile Arg Val Asn Pro His Ala Leu Ser Thr  
 290 295 300  
 Trp Met Ala Met Ile Ser Ser Lys Ser Phe Trp Ala Phe Tyr Arg Val  
 305 310 315 320  
 Tyr Leu Pro Leu Ala Val Leu Gln Met Pro Ile Lys Thr Tyr Leu Ala  
 325 330 335  
 Ile Phe Phe Leu Ala Glu Phe Val Thr Gly Trp Tyr Leu Ala Phe Asn  
 340 345 350  
 Phe Gln Val Ser His Val Ser Thr Glu Cys Gly Tyr Pro Cys Gly Asp  
 355 360 365  
 Glu Ala Lys Met Ala Leu Gln Asp Glu Trp Ala Val Ser Gln Val Lys

370	375	380
Thr Ser Val Asp Tyr Ala His Gly Ser Trp Met		Thr Thr Phe Leu Ala
385	390	395
Gly Ala Leu Asn Tyr Gln Val Val His His		Leu Phe Pro Ser Val Ser
405		410
Gln Tyr His Tyr Pro Ala Ile Ala Pro Ile Ile Val Asp Val Cys Lys		415
420	425	430
Glu Tyr Asn Ile Lys Tyr Ala Ile Leu Pro Asp Phe Thr Ala Ala Phe		435
435	440	445
Val Ala His Leu Lys His Leu Arg Asn Met Gly Gln Gln Gly Ile Ala		450
450	455	460
Ala Thr Ile His Met Gly		465
	470	

&lt;210&gt; 21

&lt;211&gt; 914

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 21

atggAACATT ttgatgcatt acttagtacc tatttcaagg cattgctagg ccctcgagat 60  
 actagagtaa aaggatgggtt tcTTCTGGAC aattatac ccacattat ctgctctgtc 120  
 atataattttac taattgtatg gctgggacca aaatacatga ggaataaaaca gccattctct 180  
 tgccggggga tttagtgggt gtataacctt ggactcacac tgctgtctct gtatatgttc 240  
 tgtgagtttag taacaggagt atgggaaggc aaatacaact tcttctgtca gggcacacgc 300  
 accgcaggag aatcagatata gaagattatc cgtgtcctct ggtggacta cttctccaaa 360  
 ctcatagaat ttatggacac ttTCTTCTTC atcctgcgca agaacaacca ccagatcacg 420  
 gtcctgcacg tctaccacca tgcctcgatg ctgaacatct ggtggttgt gatgaactgg 480  
 gtcccctgcg gccactctta ttttggtgcc acacttaata gcttcatcca cgtcctcatg 540  
 tactcttact atggTTTGTc gtcagtcctt tccatgcgtc cataccctctg gtggaaagaag 600  
 tacatcactc aggggcagct gcttcagttt gtgctgacaa tcatccagac cagctgcggg 660  
 gtcatctggc cgtgcacatt ccctcttggt tggTTgtatt tccagattgg atacattatt 720  
 tccctgatttgc ctctcttcac aaacttctac attcagacct acaacaagaa aggggcctcc 780  
 cgaaggaaag accacacgtt gggaccaccag aatgggtccg tggctgtgt gaatggacac 840  
 accaacagct ttccacccct ggaaaacaat gtgaagccaa ggaagctgcg gaaggattga 900  
 agtcaaagaa ttga 914

&lt;210&gt; 22

&lt;211&gt; 957

&lt;212&gt; DNA

&lt;213&gt; Mortierella alpina

&lt;400&gt; 22

atggAGTCGA ttgcGCCATT CCTCCATCA aagatGCCGC aagatctgtt tatggacctt 60  
 gCcAccGCTA tcggTGTCCG ggCCGCGCCC tatgtcgatc ctctcgaggc cgCgCTGGTG 120  
 gCCCAGGCCG agaagtacat cccccacgatt gtccatcaca cgCgtgggtt cctggTCGCG 180  
 gtggAGTCGC CTTGGCCCG tgagctGCCG ttgatgaacc cgTTCCACGT gCTGTTGATC 240  
 gtgCTCGCTT atttggtacG ggtctttgtt ggcatgcaga tcatgaagaa ctTTGAGCGG 300  
 ttGAGGTCA agacGTTTC gtcctgcac aactttgtc tggTCTCGAT cAGCgcCTAC 360  
 atgtGCGGTG ggatCCTGTA CGAGGTTAT caggCCAact atggactgtt tgagaacgt 420  
 gctgatCATA CCTTCAGGG tCTTCTATG gCCAAGATGA tCTGGCTCTT CTACTTCTCC 480  
 aagatcatgg agtttgcga caccatgatc atggcctca agaagaacaa ccGCCAGATC 540  
 tccttcttgc acgtttacca ccacagCTCC atttcaccat tctgggggtt ggtcacctt 600  
 gttGACCCA acggTGAAGC CTACTTCTCT gCTGCGTTGA ACTCGTTCAT CCAATGTGATC 660  
 atgtacggct actacttctt gtcggcctt ggcttcaAGC aggtgtcgtt catcaagtTC 720  
 tacatCACGC gctcgAGAT gacacAGTTc tGcatGATGt CGGTCCAGTC ttccTGGAC 780

atgtacgcca tgaaggctt tggccgcccc ggataccct tcttcatcac ggctctgctt 840  
 tggttctaca tgtggaccat gctcggtctc ttctacaact ttacagaaa gaacccaag 900  
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<220>  
 <223> Primer R0936

<400> 23  
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<210> 24  
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<220>  
 <223> Primer R0937

<400> 24  
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<210> 25  
 <211> 42  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer R0972

<400> 25  
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<210> 26  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer R0949

<400> 26  
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<210> 27  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer R0950

<400> 27

cttatactcg agtaaatggc tcgcgaggcg aagcgagtgg c 41  
 <210> 28  
 <211> 1320  
 <212> DNA  
 <213> Thraustochytrium aureum

<400> 28  
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 ggcgggtcga tcatcaagtt tctcacgacc gacggccaccg aggtgtgga cgcgacgaaac 180  
 gcgtttcgcg agtttcactg ccggcgggc aaggcgaaa agtacctaag gagectgccc 240  
 aagctcgccg cgccgagcaa gatgaagtt gacgcctaagg agcaggcccc ggcgcacgac 300  
 atcacgcgag actacgtcaa gctgcgcgag gagatggtgg ccgagggcct cttcaagccc 360  
 gcgccctcc acattgtcta caggttgcg gagatgcgag ccctgttcgc ggcctcggtc 420  
 tacctgtttt cgatgcgcgg aaacgtgttc gccacgctcg cggccatcgc agtcgggggc 480  
 atcgcgcagg gccgcgtgcgg ctggctcatg cacgagtgcg gacacttctc gatgaccggg 540  
 tacatcccgc ttgacgtgcg cctgcaggag ctggtgtacg gcgtggggtg ctcgatgtcg 600  
 gcgagctggc ggcgcgttca gcacaacaag caccacgcga cccgcagaa actcaagcac 660  
 gacgtcgacc tcgacacccct gccgctcggt gcgttcaacg agaagatcgc cgccaagggtg 720  
 cgccccggct cggtccaggc caagtggctc tcggcgcagg cgtacatttt tgccgggtg 780  
 tcctgcttcc tgggtggctc ttctggacc ctgttctgc acccgcgcca catgcccgc 840  
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 atgcactcgat tcgggtacag cgggagcgac tcggtcggtc tctacatggc caccttggc 960  
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 ctcttccgt cgctgccccca gctcaacgcg ccgcgcgtc cccgcgcgt ccgcgcctc 1200  
 ttcgagaagc acggcatgac ttacgacgag cgccgcgtacc ttaccgcgt tggcgacacg 1260  
 tttgccaacc tgcacgcgt gggccaaac gcgccagg cgccgccttag 1320

<210> 29  
 <211> 439  
 <212> PRT  
 <213> Thraustochytrium aureum

<400> 29  
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 20 25 30  
 Asp Val Thr Asn Phe Arg His Pro Gly Gly Ser Ile Ile Lys Phe Leu  
 35 40 45  
 Thr Thr Asp Gly Thr Glu Ala Val Asp Ala Thr Asn Ala Phe Arg Glu  
 50 55 60  
 Phe His Cys Arg Ser Gly Lys Ala Glu Lys Tyr Leu Lys Ser Leu Pro  
 65 70 75 80  
 Lys Leu Gly Ala Pro Ser Lys Met Lys Phe Asp Ala Lys Glu Gln Ala  
 85 90 95  
 Arg Arg Asp Ala Ile Thr Arg Asp Tyr Val Lys Leu Arg Glu Glu Met  
 100 105 110  
 Val Ala Glu Gly Leu Phe Lys Pro Ala Pro Leu His Ile Val Tyr Arg  
 115 120 125  
 Phe Ala Glu Ile Ala Ala Leu Phe Ala Ala Ser Phe Tyr Leu Phe Ser  
 130 135 140  
 Met Arg Gly Asn Val Phe Ala Thr Leu Ala Ala Ile Ala Val Gly Gly

145	150	155	160
Ile Ala Gln Gly Arg Cys Gly Trp Leu Met His Glu Cys Gly His Phe			
165	170	175	
Ser Met Thr Gly Tyr Ile Pro Leu Asp Val Arg Leu Gln Glu Leu Val			
180	185	190	
Tyr Gly Val Gly Cys Ser Met Ser Ala Ser Trp Trp Arg Val Gln His			
195	200	205	
Asn Lys His His Ala Thr Pro Gln Lys Leu Lys His Asp Val Asp Leu			
210	215	220	
Asp Thr Leu Pro Leu Val Ala Phe Asn Glu Lys Ile Ala Ala Lys Val			
225	230	235	240
Arg Pro Gly Ser Phe Gln Ala Lys Trp Leu Ser Ala Gln Ala Tyr Ile			
245	250	255	
Phe Ala Pro Val Ser Cys Phe Leu Val Gly Leu Phe Trp Thr Leu Phe			
260	265	270	
Leu His Pro Arg His Met Pro Arg Thr Ser His Phe Ala Glu Met Ala			
275	280	285	
Ala Val Ala Val Arg Val Val Gly Trp Ala Ala Leu Met His Ser Phe			
290	295	300	
Gly Tyr Ser Gly Ser Asp Ser Phe Gly Leu Tyr Met Ala Thr Phe Gly			
305	310	315	320
Phe Gly Cys Thr Tyr Ile Phe Thr Asn Phe Ala Val Ser His Thr His			
325	330	335	
Leu Asp Val Thr Glu Pro Asp Glu Phe Leu His Trp Val Glu Tyr Ala			
340	345	350	
Ala Leu His Thr Thr Asn Val Ser Asn Asp Ser Trp Phe Ile Thr Trp			
355	360	365	
Trp Met Ser Tyr Leu Asn Phe Gln Ile Glu His His Leu Phe Pro Ser			
370	375	380	
Leu Pro Gln Leu Asn Ala Pro Arg Val Ala Pro Arg Val Arg Ala Leu			
385	390	395	400
Phe Glu Lys His Gly Met Ala Tyr Asp Glu Arg Pro Tyr Leu Thr Ala			
405	410	415	
Leu Gly Asp Thr Phe Ala Asn Leu His Ala Val Gly Gln Asn Ala Gly			
420	425	430	
Gln Ala Ala Ala Lys Ala Ala			
435			

&lt;210&gt; 30

&lt;211&gt; 1338

&lt;212&gt; DNA

&lt;213&gt; Thraustochytrium aureum

&lt;400&gt; 30

gaattcacca tgggtcgccgg	agcacaggga gagccaaggc	aggccacaga gctgaagagc	60
agcccaagtg agcagcgtaa	ggtgttgctc attgacgggc	agctgtacga tgcaaccaac	120
tccaggcattc ctggtggtctc	catcatcaaa tatttgtca	ccgatggcaa ggaggttagtt	180
gatgcaaccg aagcgtaaa	ggagttccac tgcagatcc	cgaaggcggt caagtacotc	240
aactccctgc caaagatcga	cggcccaatc aagtacaat	acgacgc当地 ggagcgaggct	300
cggccatgaca aactcacgag	ggagtatgtt gctctcccg	aacagtc当地 caaggagggta	360
tactttgacc ccagccccgt	ccacatttac tacagatgc	ccgagttggc agccatgttc	420
gctctctcg	tctacctttt ctccttcaag	ggtaacgtca tggccactat tgctgcccattc	480
gtgattgggg ggtgcgtgca	gggtcggtgt gggtggtca	tgcataaagc tggccactac	540
agcatgaccc gaaacatccc	tgttgacttg cgccttcaag	agttttgtt cggatttggg	600
tgtggcatga gcggggcttg	gtggagaagc cagcacaaca	agcaccacgc caccffffcaa	660
aagctcaagc atgacgttga	tttggacact cttccttgc	tcgccttggaa cgagaaaatt	720

gccccgtcgcg	tcaagccagg	tagcttccag	gcaaagtggc	ttcatctcca	gggatacatc	780
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cacatgatcc	gcaccaagcg	caacttcgag	atattttctg	tcgctctgct	ctacgtatgc	900
tggttctcgc	ttcttttgag	catgggctac	actgtcggag	agtctctggg	tctctatgt	960
cttacttttgc	gacttggctg	tacctacatc	tttacgcatt	ttgctgttaag	ccacacccac	1020
ttgccagttgt	ccgaggagga	cgagttacctg	cactgggtcg	agtacgctgc	gctgcacacc	1080
acgaacgttg	ccatcgactc	gtacgttgc	acctggctga	tgagctacct	caacttcag	1140
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gtcaagaaaac	ttttcgagga	caatggctcg	gtatacga	ccgctcata	cgtccaggcg	1260
ctcaaggata	ccttcggcaa	cctacacgaa	gtgggcgtca	acgctggcca	agctgccaag	1320
agcgagtaag	atctcgag					1338

&lt;210&gt; 31

&lt;211&gt; 439

&lt;212&gt; PRT

&lt;213&gt; Thraustochytrium aureum

&lt;400&gt; 31

Met	Gly	Arg	Gly	Ala	Gln	Gly	Glu	Pro	Arg	Gln	Ala	Thr	Glu	Leu	Lys
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Ser	Ser	Pro	Ser	Glu	Gln	Arg	Lys	Val	Leu	Leu	Ile	Asp	Gly	Gln	Leu
				20				25				30			
Tyr	Asp	Ala	Thr	Asn	Phe	Arg	His	Pro	Gly	Gly	Ser	Ile	Ile	Lys	Tyr
				35				40				45			
Leu	Cys	Thr	Asp	Gly	Lys	Glu	Val	Val	Asp	Ala	Thr	Glu	Ala	Tyr	Lys
				50				55				60			
Glu	Phe	His	Cys	Arg	Ser	Ser	Lys	Ala	Val	Lys	Tyr	Leu	Asn	Ser	Leu
				65				70				75			80
Pro	Lys	Ile	Asp	Gly	Pro	Ile	Lys	Tyr	Lys	Tyr	Asp	Ala	Lys	Glu	Gln
				85				90				95			
Ala	Arg	His	Asp	Lys	Leu	Thr	Arg	Glu	Tyr	Val	Ala	Leu	Arg	Glu	Gln
				100				105				110			
Leu	Val	Lys	Glu	Gly	Tyr	Phe	Asp	Pro	Ser	Pro	Leu	His	Ile	Ile	Tyr
				115				120				125			
Arg	Cys	Ala	Glu	Leu	Ala	Ala	Met	Phe	Ala	Leu	Ser	Phe	Tyr	Leu	Phe
				130				135				140			
Ser	Phe	Lys	Gly	Asn	Val	Met	Ala	Thr	Ile	Ala	Ile	Val	Ile	Gly	
				145				150				155			160
Gly	Cys	Val	Gln	Gly	Arg	Cys	Gly	Trp	Leu	Met	His	Glu	Ala	Gly	His
				165				170				175			
Tyr	Ser	Met	Thr	Gly	Asn	Ile	Pro	Val	Asp	Leu	Arg	Leu	Gln	Glu	Phe
				180				185				190			
Leu	Tyr	Gly	Ile	Gly	Cys	Gly	Met	Ser	Gly	Ala	Trp	Trp	Arg	Ser	Gln
				195				200				205			
His	Asn	Lys	His	His	Ala	Thr	Pro	Gln	Lys	Leu	Lys	His	Asp	Val	Asp
				210				215				220			
Leu	Asp	Thr	Leu	Pro	Leu	Val	Ala	Trp	Asn	Glu	Lys	Ile	Ala	Arg	Arg
				225				230				235			240
Val	Lys	Pro	Gly	Ser	Phe	Gln	Ala	Lys	Trp	Leu	His	Leu	Gln	Gly	Tyr
				245				250				255			
Ile	Phe	Ala	Pro	Val	Ser	Cys	Leu	Leu	Val	Gly	Leu	Phe	Trp	Thr	Leu
				260				265				270			
Tyr	Leu	His	Pro	Arg	His	Met	Ile	Arg	Thr	Lys	Arg	Asn	Phe	Glu	Ile
				275				280				285			
Phe	Ser	Val	Ala	Leu	Arg	Tyr	Val	Cys	Trp	Phe	Ser	Leu	Leu	Leu	Ser
				290				295				300			
Met	Gly	Tyr	Thr	Val	Gly	Glu	Ser	Leu	Gly	Leu	Tyr	Val	Leu	Thr	Phe

305	310	315	320
Gly Leu Gly Cys Thr Tyr Ile Phe Thr His Phe Ala Val Ser His Thr			
325	330	335	
His Leu Pro Val Ser Glu Glu Asp Glu Tyr Leu His Trp Val Glu Tyr			
340	345	350	
Ala Ala Leu His Thr Thr Asn Val Ala Ile Asp Ser Tyr Val Val Thr			
355	360	365	
Trp Leu Met Ser Tyr Leu Asn Phe Gln Ile Glu His His Leu Phe Pro			
370	375	380	
Cys Cys Pro Gln Phe Arg His Pro Ala Ile Ser Ser Arg Val Lys Lys			
385	390	395	400
Leu Phe Glu Asp Asn Gly Leu Val Tyr Asp Ala Arg Ser Tyr Val Gln			
405	410	415	
Ala Leu Lys Asp Thr Phe Gly Asn Leu His Glu Val Gly Val Asn Ala			
420	425	430	
Gly Gln Ala Ala Lys Ser Glu			
435			

&lt;210&gt; 32

&lt;211&gt; 1381

&lt;212&gt; DNA

&lt;213&gt; Thraustochytrium aureum

&lt;400&gt; 32

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agctccagaa ggccaagtgg gaggatgtt ttcgcataa tggagtcgaa tacgacgtca	120
cggactatct cagaaaacac cctggtgca gctgtatcaa gtacgggctt gccaacacccg	180
gctgtatgc cacgtccctc tttgaagcgt tccacatgctg ctcaagaag gctcagatgg	240
tgcgtatgc tctcccaaag cgtgctccgg tcctcgagat ccagccaaac cagttccag	300
aggagcagac caaggaggcg gagatgctgc gtgatttaa aaaattttag gatgagattc	360
gccgggatgg attgatggaa ctttccttct ggcacatgcgc ttacagatta tcagagctt	420
taggtatgtt cacgtctggc ctctacctct tctcgtaaa cactcctctg tctattgt	480
ctgggtcct cgtccacggc ctcttggc tattctgtt atgggtccag catgaggcag	540
gccacggctc cttttttac agcctttggt gggcaagcg tgtacaggcc atgttgcgt	600
ggtttggctc aggaacatcc ggcacatgtt ggaacatgtat gcacaacaag catcatgt	660
ccacccaaaa ggttcatcac gaccttgaca ttgacacaac tcctttgtt gctttcttca	720
acactgcatt tgagaaaaac agatggaagg gctttccaa ggcttggc cgctttcagg	780
ctttcacgtt cattcctgtc accagcggca tgatcgatcat gctgttctgg ctgtttttc	840
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gccacattgt ggcacatct ctcttccacc ttgtgaccgg ctggagagc ctcgtgtcat	960
gctacattgt tgggtatgg gctgtcatgt ggggtccgg tatgtatgg tttggccact	1020
tttcgtctc ccacactcat atggacatgtt gggggcggc cgtgcataag aactgggtca	1080
ggtacgtgt tgaccacatgtt gttgacatca gcccataccaa cccgctcggt tgctgggtca	1140
tgggttacat caacatgcg accatccacc acttgtggcc tgccatgcccc cagtaccacc	1200
agggtcgagggt ctcacgccc tttggccatct tcgccccaaa acacggcctc aactaccgcg	1260
tcgtctctta ctttgaggct tggccctga tgctccaaa tcttgctgac gtcgggttccc	1320
actaccatga gaacggtgtc aagcgcgc ccaagaaagc caaggcgcag tagaaagcta	1380
t	1381

&lt;210&gt; 33

&lt;211&gt; 456

&lt;212&gt; PRT

&lt;213&gt; Thraustochytrium aureum

&lt;400&gt; 33

Met Gly Arg Gly Gly Glu Lys Ser Glu Val Asp Gln Val Gln Pro Gln			
1	5	10	15

Lys Thr Glu Gln Leu Gln Lys Ala Lys Trp Glu Asp Val Val Arg Ile  
     20                 25                 30  
 Asn Gly Val Glu Tyr Asp Val Thr Asp Tyr Leu Arg Lys His Pro Gly  
     35                 40                 45  
 Gly Ser Val Ile Lys Tyr Gly Leu Ala Asn Thr Gly Ala Asp Ala Thr  
     50                 55                 60  
 Ser Leu Phe Glu Ala Phe His Met Arg Ser Lys Lys Ala Gln Met Val  
     65                 70                 75                 80  
 Leu Lys Ser Leu Pro Lys Arg Ala Pro Val Leu Glu Ile Gln Pro Asn  
     85                 90                 95  
 Gln Leu Pro Glu Glu Gln Thr Lys Glu Ala Glu Met Leu Arg Asp Phe  
     100                105               110  
 Lys Lys Phe Glu Asp Glu Ile Arg Arg Asp Gly Leu Met Glu Pro Ser  
     115                120               125  
 Phe Trp His Arg Ala Tyr Arg Leu Ser Glu Leu Val Gly Met Phe Thr  
     130                135               140  
 Leu Gly Leu Tyr Leu Phe Ser Leu Asn Thr Pro Leu Ser Ile Ala Ala  
     145                150               155               160  
 Gly Val Leu Val His Gly Leu Phe Gly Ala Phe Cys Gly Trp Cys Gln  
     165                170               175  
 His Glu Ala Gly His Gly Ser Phe Phe Tyr Ser Leu Trp Trp Gly Lys  
     180                185               190  
 Arg Val Gln Ala Met Leu Ile Gly Phe Gly Leu Gly Thr Ser Gly Asp  
     195                200               205  
 Met Trp Asn Met Met His Asn Lys His His Ala Ala Thr Gln Lys Val  
     210                215               220  
 His His Asp Leu Asp Ile Asp Thr Thr Pro Phe Val Ala Phe Phe Asn  
     225                230               235               240  
 Thr Ala Phe Glu Lys Asn Arg Trp Lys Gly Phe Ser Lys Ala Trp Val  
     245                250               255  
 Arg Phe Gln Ala Phe Thr Phe Ile Pro Val Thr Ser Gly Met Ile Val  
     260                265               270  
 Met Leu Phe Trp Leu Phe Phe Leu His Pro Arg Arg Val Val Gln Lys  
     275                280               285  
 Lys Asn Phe Glu Glu Gly Phe Trp Met Leu Ser Ser His Ile Val Arg  
     290                295               300  
 Thr Tyr Leu Phe His Leu Val Thr Gly Trp Glu Ser Leu Ala Ala Cys  
     305                310               315               320  
 Tyr Leu Val Gly Tyr Trp Ala Cys Met Trp Val Ser Gly Met Tyr Leu  
     325                330               335  
 Phe Gly His Phe Ser Leu Ser His Thr His Met Asp Ile Val Glu Ala  
     340                345               350  
 Asp Val His Lys Asn Trp Val Arg Tyr Ala Val Asp His Thr Val Asp  
     355                360               365  
 Ile Ser Pro Ser Asn Pro Leu Val Cys Trp Val Met Gly Tyr Leu Asn  
     370                375               380  
 Met Gln Thr Ile His His Leu Trp Pro Ala Met Pro Gln Tyr His Gln  
     385                390               395               400  
 Val Glu Val Ser Arg Arg Phe Ala Ile Phe Ala Lys Lys His Gly Leu  
     405                410               415  
 Asn Tyr Arg Val Val Ser Tyr Phe Glu Ala Trp Arg Leu Met Leu Gln  
     420                425               430  
 Asn Leu Ala Asp Val Gly Ser His Tyr His Glu Asn Gly Val Lys Arg  
     435                440               445  
 Ala Pro Lys Lys Ala Lys Ala Gln  
     450                455

<210> 34  
<211> 1329  
<212> DNA  
<213> Isochrysis galbana

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atcgatgctg	aaaaggagat	gatcatcaac	ggccgcgtgt	atgacgtgtc	gtcatttgc	180
aaggccgacc	caggtggctc	ggtgatcaag	ttccagctgg	gcgcgcacgc	gagcgacgcg	240
tacaacaact	ttcacgtccg	ctccaagaag	gcccagaaga	tgctgtattc	gctcccgcc	300
cgccggccg	aggccggcta	cgcccaggac	gacatctccc	gcgactttga	gaagctgcgc	360
ctcgagctga	aggaggaggg	ctacttcgag	cccaacctgg	tgcacgttag	ctacagggtgt	420
gtggagggttc	ttggccatgta	ctgggctggc	gtccagctca	tctggctccg	gtactgggtc	480
ctcgccgcga	tcgtggccgg	cattgcgcag	ggccgctcg	gctggctcca	gcatgagggt	540
gggcactact	cgctcaccgg	caacatcaag	atgcaccggc	atctgcagat	ggccatctat	600
gggcttggct	gcccgcgtgc	gggctgtac	tggcgcaacc	agcacaacaa	gcaccacgccc	660
acgcccgcaga	agctcgggac	cgaccccgac	ctgcagacga	tgccgctgg	ggcccttccac	720
aagatcgctg	gcgcacaggc	gcccggcaag	ggcaaggcg	ggctggcg	gcaggcgccg	780
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gtgctgtggc	acctggcctt	tggccaccc	gggctgtga	gtcgctccg	cctgtacgcc	960
ttttacgtgg	ccgtggccgg	cacctacatc	ttcaccaact	tcggcgctc	gcacacccac	1020
aaggacgtcg	tcccgcccc	caagcacatc	tctggggac	tctactcg	caaccacacg	1080
accaactgtc	ccgactcgcc	cttgcacac	tggggatgg	cctacccaa	cttccagatc	1140
gaggaccaccc	tctcccg	gatgccgcag	tacaaccacc	ccaagatcg	cccgccgggt	1200
cgccgcgtct	tcgagaagca	cggggctcgag	tatgacgtcc	ggccataacct	ggagtgttt	1260
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acgcactag						1329

<210> 35  
<211> 442  
<212> PRT  
<213> Isochrysis galbana

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<400> 35
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Thr Leu Pro Arg Glu Tyr His Gly Ala Thr Asn Asp Ser Arg Ser Glu
      20          25          30
Ala Ala Asp Val Thr Val Ser Ser Ile Asp Ala Glu Lys Glu Met Ile
      35          40          45
Ile Asn Gly Arg Val Tyr Asp Val Ser Ser Phe Val Lys Arg His Pro
      50          55          60
Gly Gly Ser Val Ile Lys Phe Gln Leu Gly Ala Asp Ala Ser Asp Ala
      65          70          75          80
Tyr Asn Asn Phe His Val Arg Ser Lys Lys Ala Asp Lys Met Leu Tyr
      85          90          95
Ser Leu Pro Ser Arg Pro Ala Glu Ala Gly Tyr Ala Gln Asp Asp Ile
      100         105         110
Ser Arg Asp Phe Glu Lys Leu Arg Leu Glu Leu Lys Glu Glu Gly Tyr
      115         120         125
Phe Glu Pro Asn Leu Val His Val Ser Tyr Arg Cys Val Glu Val Leu
      130         135         140
Ala Met Tyr Trp Ala Gly Val Gln Leu Ile Trp Ser Gly Tyr Trp Phe
      145         150         155         160
Leu Gly Ala Ile Val Ala Gly Ile Ala Gln Gly Arg Cys Gly Trp Leu

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Gln	His	Glu	Gly	Gly	His	Tyr	Ser	Leu	Thr	Gly	Asn	Ile	Lys	Ile	Asp
165									170					175	
									180					180	
Arg	His	Leu	Gln	Met	Ala	Ile	Tyr	Gly	Leu	Gly	Cys	Gly	Met	Ser	Gly
									185					190	
195									195	200				205	
Cys	Tyr	Trp	Arg	Asn	Gln	His	Asn	Lys	His	His	Ala	Thr	Pro	Gln	Lys
									210	215				220	
Leu	Gly	Thr	Asp	Pro	Asp	Leu	Gln	Thr	Met	Pro	Leu	Val	Ala	Phe	His
									225	230				235	
Lys	Ile	Val	Gly	Ala	Lys	Ala	Arg	Gly	Lys	Gly	Lys	Ala	Trp	Leu	Ala
									245	250				255	
Trp	Gln	Ala	Pro	Leu	Phe	Phe	Gly	Gly	Ile	Ile	Cys	Ser	Leu	Val	Ser
									260	265				270	
Phe	Gly	Trp	Gln	Phe	Val	Leu	His	Pro	Asn	His	Ala	Leu	Arg	Val	His
									275	280				285	
Asn	His	Leu	Glu	Leu	Ala	Tyr	Met	Gly	Leu	Arg	Tyr	Val	Leu	Trp	His
									290	295				300	
Leu	Ala	Phe	Gly	His	Leu	Gly	Leu	Leu	Ser	Ser	Leu	Arg	Leu	Tyr	Ala
									305	310				315	
Phe	Tyr	Val	Ala	Val	Gly	Gly	Thr	Tyr	Ile	Phe	Thr	Asn	Phe	Ala	Val
									325	330				335	
Ser	His	Thr	His	Lys	Asp	Val	Val	Pro	Pro	Thr	Lys	His	Ile	Ser	Trp
									340	345				350	
Ala	Leu	Tyr	Ser	Ala	Asn	His	Thr	Thr	Asn	Cys	Ser	Asp	Ser	Pro	Phe
									355	360				365	
Val	Asn	Trp	Trp	Met	Ala	Tyr	Leu	Asn	Phe	Gln	Ile	Glu	His	His	Leu
									370	375				380	
Phe	Pro	Ser	Met	Pro	Gln	Tyr	Asn	His	Pro	Lys	Ile	Ala	Pro	Arg	Val
									385	390				395	
Arg	Ala	Leu	Phe	Glu	Lys	His	Gly	Val	Glu	Tyr	Asp	Val	Arg	Pro	Tyr
									405	410				415	
Leu	Glu	Cys	Phe	Arg	Val	Thr	Tyr	Val	Asn	Leu	Leu	Ala	Val	Gly	Asn
									420	425				430	
Pro	Glu	His	Ser	Tyr	His	Glu	His	Thr	His						
									435	440					

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&lt;211&gt; 36

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Primer RO838

&lt;221&gt; misc\_feature

&lt;222&gt; (7)...(7)

&lt;223&gt; v = a or g or c at position 7

&lt;221&gt; misc\_feature

&lt;222&gt; (10)...(10)

&lt;223&gt; r = g or a at position 10

&lt;221&gt; misc\_feature

&lt;222&gt; (13)...(13)

&lt;223&gt; s = g or c at position 13

&lt;221&gt; misc\_feature

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<223> r = g or a at position 16

<221> misc_feature
<222> (19)...(19)
<223> r = g or a at position 19

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<223> y = t/u or c at position 22

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<223> r = g or a at position 25

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